

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/574,018A
Source: IFW
Date Processed by STIC: 12/5/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/574,018A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics**
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 ☒ **Misaligned Amino**
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 ☐ **PatentIn 2.0**
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 ☐ **Skipped Sequences**
 (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 ☐ **Skipped Sequences**
 (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 ☐ **Use of n's or Xaa's**
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 ☒ **Invalid <213>**
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 ☐ **PatentIn 2.0**
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 12/05/2006

PATENT APPLICATION: US/10/574,018A

TIME: 10:04:55

Input Set : N:\RJAVED\10574018A.txt

Output Set: N:\CRF4\12052006\J574018A.raw

3 <110> APPLICANT: The Hospital for Sick Children
 5 <120> TITLE OF INVENTION: Method of in situ Detection of Proteins Using
 6 Aptamers
 8 <130> FILE REFERENCE: 3206-276 LAB
 10 <140> CURRENT APPLICATION NUMBER: 10/574,018A
 C--> 11 <141> CURRENT FILING DATE: 2006-03-29
 14 <150> PRIOR APPLICATION NUMBER: U.S. 60/506776
 15 <151> PRIOR FILING DATE: 2003-09-30
 17 <160> NUMBER OF SEQ ID NOS: 9
 19 <170> SOFTWARE: PatentIn Ver. 3.1

see pp 1-2
 Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

50 <210> SEQ ID NO: 3
 51 <211> LENGTH: 12
 52 <212> TYPE: PRT
 53 <213> ORGANISM: Peptide
 55 <400> SEQUENCE: 3
 57 Met Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly
 E--> 58 1 ~~5~~ ~~5~~ ~~10~~ ~~10~~ *invalid response. see item 10 on Error summary sheet*
 61 <210> SEQ ID NO: 4
 62 <211> LENGTH: 73
 63 <212> TYPE: DNA
 64 <213> ORGANISM: Artificial
 66 <220> FEATURE:
 67 <223> OTHER INFORMATION: Primer
 69 <400> SEQUENCE: 4
 E--> 71 ggggttttaag cttaccatgg gatataccta tgatgtgcca gactacgcgg gaatgtctag 60 attagataaa
 E--> 72 agt 73
misaligned numbering. see item 3 on Error summary sheet.
insert a hard return

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/574,018A

DATE: 12/05/2006
TIME: 10:04:56

Input Set : N:\RJAVED\10574018A.txt
Output Set: N:\CRF4\12052006\J574018A.raw

Fy I

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:4; Line(s) 71

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823 (b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,4,5,6,7,8,9

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/574,018A

DATE: 12/05/2006

TIME: 10:04:56

Input Set : N:\RJAVED\10574018A.txt

Output Set: N:\CRF4\12052006\J574018A.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:58 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:71 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:72 M:254 E: No. of Bases conflict, LENGTH:Input:73 Counted:3 SEQ:4
L:72 M:252 E: No. of Seq. differs, <211> LENGTH:Input:73 Found:3 SEQ:4